

**FUZZY AND NEURAL MODELS FOR
THE ACCUMULATION PROCESS OF THE PROTEIC MASS FROM
SUPERIOR MUSHROOM MICELIUM OF POLYPORUS TYPE**

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Abstract: This paper deals with the possibility of modelling the accumulation process of the proteic mass from superior mushroom mycelium of *Polyporus* type by fuzzy and neural techniques. Two models are considered for the main parameter of the process (the biomass specific growth rate): the first is a fuzzy model and the second is a neural one. The simulation results are compared to the real data given by the Food Industry Institute from Bucharest.

Keywords: Biotechnological Process, Fuzzy rules, neural network, biomass specific growth rate

1. INTRODUCTION

It is very well known that the biotechnological processes are complex and strong non-linear. The difficulty to model and to control such processes is bigger in the case of discontinuous processes. They are totally isolated from the outside environment. During the process no additional substrate is fed from the outside, the microorganisms population growing only from the substrate supplied at the beginning of the batch. A number of uncertainties arises right from the beginning of the process with respect to the substrate preparation and nature (the composition of the natural substrates is not precisely known). Generally, these initial batch-preparation operations cannot be mathematically formalized thus generating major problems in the process modelling and the synthesis of the control system.

The classic modelling techniques refer only to the metabolic process. In the specialty literature is known the method based on mass balanced equations (Bastin and Dochain, 1990). The result consists in the obtaining of a structural-functioning model, based on the kinetics and transport dynamics of the components involved in the process. Another method is to describe the biosynthesis process considering

the main zones in its evolution. Thus every phase of the population evolution is described by a simple model. Other specialists have used artificial intelligence techniques (knowledge-based systems, fuzzy, neural) for modelling the biosynthesis processes. Are well known the papers (Bettenhausen, *et al.*, 1993; Aarts, *et al.*, 1989; Aarts, *et al.*, 1991; Konstandinov, *et al.*, 1992), which developed expert systems to model and control the discontinuous biotechnological processes.

This paper does consider a biomass producing process (the accumulation process of the proteic mass from superior mushroom mycelium of *Polyporus* type) and combines two modelling methods: mass balanced equations and artificial intelligence techniques. In the mathematical equations of the model, the main parameters are expressed by fuzzy and neural network models. The authors started with the main parameter, the viable biomass specific growth rate, expressed as a function of to variables (substrates S_1 and S_2).

The paper is structured in 5 sections: in section 2 is presented the structural-functioning model of the accumulation process of the proteic mass from superior mushroom mycelium of *Polyporus* type

sections 3 and 4 refer to the fuzzy, respective neural model, and the last section is dedicated to the conclusions.

2. THE STRUCTURAL-FUNCTIONING MODEL OF THE MASS PROTEIC ACCUMULATION PROCESS

Considering the curves plotted according to the experimental data (figure 1), two conclusions have resulted:

- the biomass accumulation dynamics in the culture environment is represented by a curve, which has two growth phases separated by a decay (adaptation) stage. This suggests a successive usage of two substrates. The consuming of the second substrate (s_2) is made only after the first substrate (s_1) has been exhausted;
- the lag phase is missing or it is very small. The first growth phase is almost linear, which concludes that in the kinetic equation there is a term non-proportional to the biomass x .

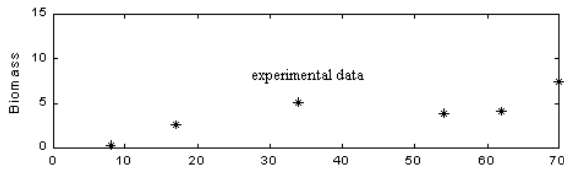


Fig. 1. Biomass (experimental data)

Thus, it has been admitted that the accumulation process of the proteic mass from superior mushroom mycelium of *Polyporus* type in a batch bioreactor can be represented as follows:

$$\dot{x} = k_1(x + k_4) + k_2(x + k_5) - k_3x \quad (1)$$

$$\dot{s}_1 = -k_1(x + k_4) \quad (2)$$

$$\dot{s}_2 = -k_2(x + k_5) \quad (3)$$

where x represents the biomass, s_1 and s_2 are the substrates used in the two successive growth phases and k_i ($i=1, \dots, 5$) represents the kinetic coefficients of the reactions. For the coefficient k_1 (biomass growth rate) it has been adopted the following expression:

$$k_1 = k_{10} \frac{s_1}{k_{s_1} + s_1} \quad (4)$$

For the calculus of the coefficient k_2 (the second biomass growth rate) two variants have been proposed:

- a. substrate s_2 begins to be consumed after the substrate s_1 decreases under a specific threshold value (s_{10}):

$$k_2 = \begin{cases} 0, & s_1 > s_{10} \\ k_2 = k_{20} \frac{s_2}{k_{s_2} + s_2}, & s_1 \leq s_{10} \end{cases} \quad (5)$$

- b. a continuous transition from the substrate s_1 to substrate s_2 consuming:

$$k_2 = k_{20} \frac{s_2}{k_{s_2} + s_2} \cdot \frac{k_{s_1}^*}{k_{s_1}^* + s_1} \quad (6)$$

where $k_{s_1}^*$ is the value of the substrate s_1 when k_2 is diminished to a half.

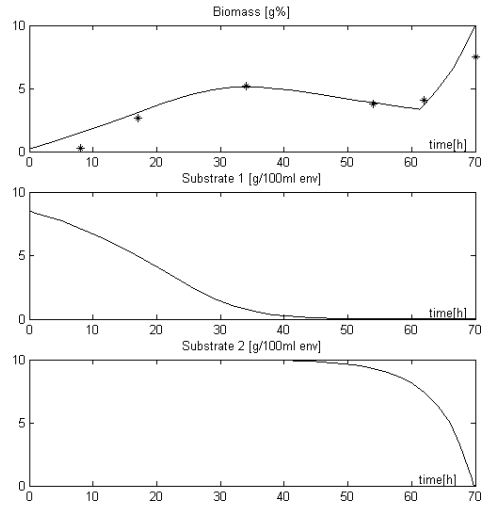


Fig. 2: Simulation result - variant a

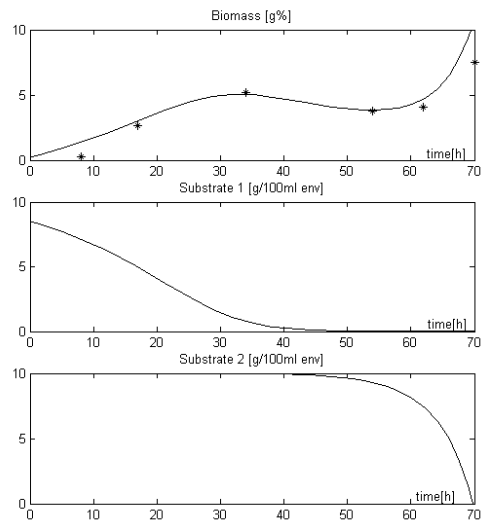


Fig. 3: Simulation result - variant b

The result of the simulations (variants *a* and *b*) are presented in figures 2 and 3. The coefficients values and initial conditions used in simulations are the following:

- a. $k_{10}=0.085$, $k_{s1}=3$, $k_{20}=0.125$, $k_{s2}=0.01$, $k_3=0.02$, $k_4=2$, $k_5=1$, $s_{10}=0.0055$, $x(0)=0.25$, $s_1(0)=7.5$, $s_2(0)=11$;
- b. $k_{10}=0.1$, $k_{s1}=3$, $k_{20}=0.2$, $k_{s2}=0.01$, $k_3=0.03$, $k_4=1.5$, $k_5=0.5$, $k_{s1}^*=0.0028$, $x(0)=0.25$, $s_1(0)=8.5$, $s_2(0)=10$.

3. THE FUZZY MODEL OF THE MASS PROTEIC ACCUMULATION PROCESS

In this section, the model of the accumulation process of the proteic mass from superior mushroom mycelium of *Polyporus* type is given by the equations (1) – (3), where the biomass specific growth rate is generated by a fuzzy block. The inputs of the fuzzy block are the two substrates S_1 and S_2 and the biomass specific growth rate, $\mu(S_1, S_2)$ is the output. It has been considered that the two substrates are consumed with the same rate. The membership functions of the inputs and output are presented in figure 4.

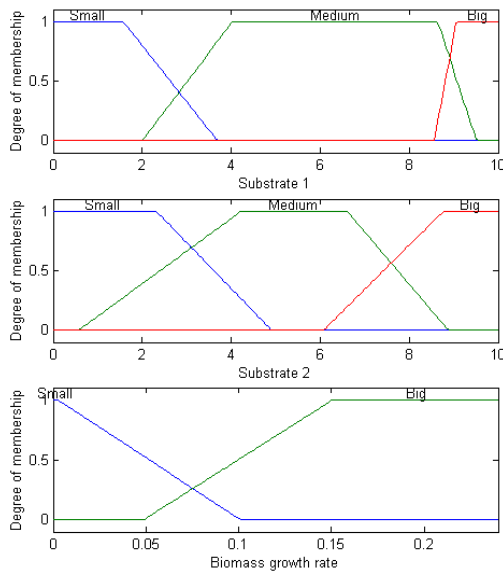


Fig. 4. The membership functions of the fuzzy block inputs (substrates S_1 and S_2) and output (the biomass specific growth rate)

The fuzzy block implements the dependence of the biomass specific growth rate of the two substrates and it has to express the fact that the substrates S_1 and S_2 are consumed one by one (the first is consumed the substrates S_1).

The rules of the fuzzy block are the following:

- R1. IF (S_1 is Big) AND (S_2 is Big) THEN (μ is Small)
- R2. IF (S_1 is Medium) AND (S_2 is Big) THEN (μ is Big)
- R3. IF (S_1 is Small) AND (S_2 is Big) THEN (μ is Small)
- R4. IF (S_1 is Small) AND (S_2 is Medium) THEN (μ is Big)
- R5. IF (S_1 is Small) AND (S_2 is Small) THEN (μ is Small)

A part of the complete rule-base is never used in the inference mechanism because the two substrates cannot take values in these regions. This is why only 5 rules ($R_1 - R_5$) are used in the inference mechanism. The response surface is presented in figure 5.

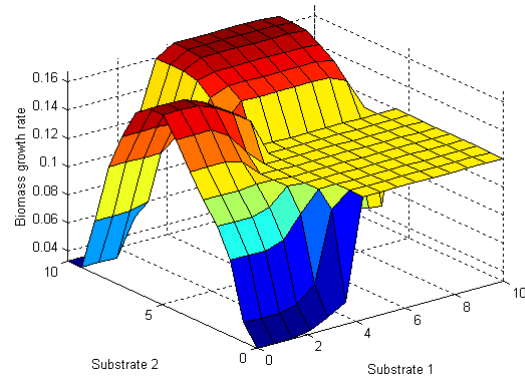


Fig. 5. The response surface of the fuzzy block

The simulations results are shown in figure 6.

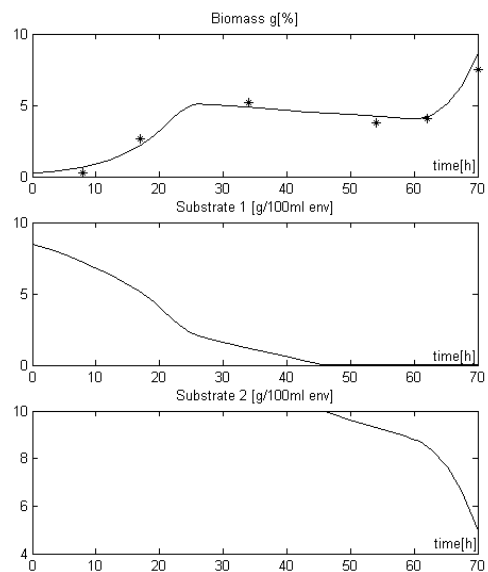


Fig. 6. The simulation results of the fuzzy model

4. THE NEURAL MODEL OF THE MASS PROTEIC ACCUMULATION PROCESS

The same variable (the biomass specific growth rate) has been modelled by a two layers feed-forward neural network. The first layer contains two neurons and the second one neuron, as in figure 7. The activation function is *purelin* and the neural network training has been made using the back-propagation algorithm.

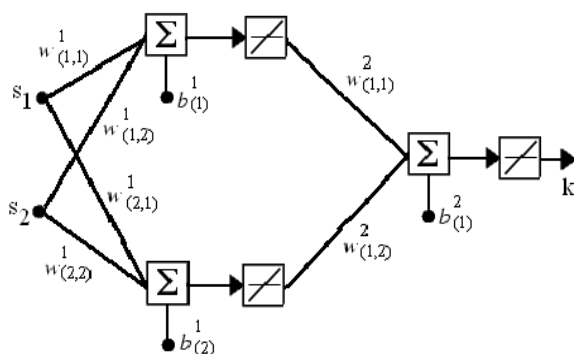


Fig. 7. The neural network structure

The simulation results of the neural model are shown in figure 8.

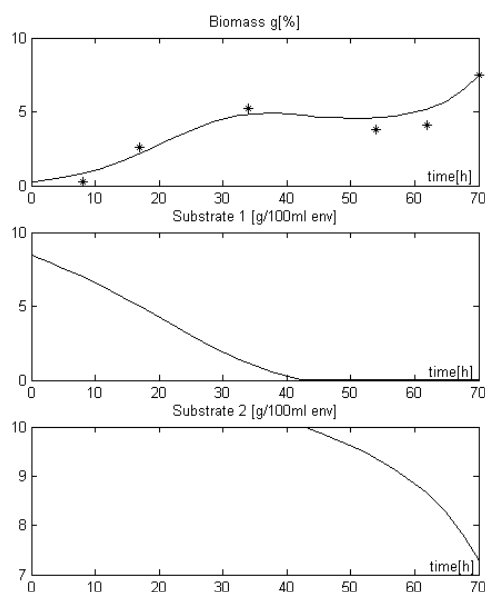


Fig. 8. The simulation results of the neural model

5. CONCLUSIONS

From the paper the following conclusions can be drawn:

1. This paper deals with the possibility to model by fuzzy and neural techniques the main parameter of a biotechnological process, the biomass

specific growth rate.

2. The dependence modelled by fuzzy and neural techniques is multiple (μ depends on the substrates S_1 and S_2). The model can be easily determined using the expertise of the operator and it quantifies the uncertainties in the measure or the calculus of this parameter.
3. The neural network used for the biomass growth rate model must be very well trained, otherwise the process could become unstable.
4. The simulation results of fuzzy and neural models shows a good correspondence with the experimental data, given by the Food Industry Institute from Bucharest.

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